

SEQUENCE LISTING

<110> ANDERSON, DARRELL R.
HANNA, NABIL
BRAMS, PETER
HEARD, CHERYL

<120> TREATMENT OF CROHN'S DISEASE USING ANTI-CD80 ANTIBODIES THAT
DO NOT INHIBIT THE BINDING OF CD80 ANTIGEN TO CTLA-4

<130> 37003-275681

<140> 09/576,424

<141> 2000-05-22

<150> PCT/US97/19906

<151> 1997-10-29

<150> 08/746,361

<151> 1996-11-08

<150> 08/487,550

<151> 1995-06-07

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 705

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(702)

<400> 1

atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc cca	48
Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro	
1 5 10 15	
ggt gca cga tgt gcc tat gaa ctg act cag cca ccc tcg gtg tca gtg	96
Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val	
20 25 30	
tcc cca gga cag acg gcc agg atc acc tgt ggg gga gac aac agt aga	144
Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg	
35 40 45	
aat gaa tat gtc cac tgg tac cag cag aag cca gcg cgg gcc cct ata	192
Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile	
50 55 60	
ctg gtc atc tat gat gat agt gac cgg ccc tca ggg atc cct gag cga	240
Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg	
65 70 75 80	
ttc tct ggc tcc aaa tca ggg aac acc gcc acc ctg acc atc aac ggg	288
Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly	
85 90 95	

gtc gag gcc ggg gat gag gct gac tat tac tgt cag gtg tgg gac agg	336
Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg	
100 105 110	
gct agt gat cat ccg gtc ttc gga gga ggg acc cgg gtg acc gtc cta	384
Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu	
115 120 125	
ggt cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct	432
Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser	
130 135 140	
gag gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac	480
Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp	
145 150 155 160	
ttc tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc	528
Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro	
165 170 175	
gtc aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac	576
Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn	
180 185 190	
aag tac gcg gcc agc agc tac ctg agc ctg acg cct gag cag tgg aag	624
Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys	
195 200 205	
tcc cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg	672
Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val	
210 215 220	
gag aag aca gtg gcc cct aca gaa tgt tca tga	705
Glu Lys Thr Val Ala Pro Thr Glu Cys Ser	
225 230	
<210> 2	
<211> 234	
<212> PRT	
<213> Homo sapiens	
<400> 2	
Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro	
1 5 10 15	
Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val	
20 25 30	
Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg	
35 40 45	
Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile	
50 55 60	
Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg	
65 70 75 80	
Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly	

85					90					95					
Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Arg
			100					105					110		
Ala	Ser	Asp	His	Pro	Val	Phe	Gly	Gly	Gly	Thr	Arg	Val	Thr	Val	Leu
		115					120					125			
Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser
	130					135					140				
Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp
145					150					155					160
Phe	Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro
				165					170					175	
Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn
			180					185					190		
Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys
		195					200					205			
Ser	His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val
	210					215					220				
Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser						
225					230										

<210> 3
 <211> 1431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1428)

<400> 3																
atg	aaa	cac	ctg	tgg	ttc	ttc	ctc	ctc	ctg	gtg	gca	gct	ccc	aga	tgg	48
Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	
1				5					10					15		
gtc ctg tcc cag gtg aag ctg cag cag tgg ggc gaa gga ctt ctg cag															96	
Val	Leu	Ser	Gln	Val	Lys	Leu	Gln	Gln	Trp	Gly	Glu	Gly	Leu	Leu	Gln	
			20				25						30			
cct tcg gag acc ctg tcc cgc acc tgc gtt gtc tct ggt ggc tcc atc															144	
Pro	Ser	Glu	Thr	Leu	Ser	Arg	Thr	Cys	Val	Val	Ser	Gly	Gly	Ser	Ile	
		35					40					45				
agc ggt tac tac tac tgg acc tgg atc cgc cag acc cca ggg agg gga															192	
Ser	Gly	Tyr	Tyr	Tyr	Trp	Thr	Trp	Ile	Arg	Gln	Thr	Pro	Gly	Arg	Gly	
	50					55				60						
ctg gag tgg att ggc cat att tat ggt aat ggt gcg acc acc aac tac															240	
Leu	Glu	Trp	Ile	Gly	His	Ile	Tyr	Gly	Asn	Gly	Ala	Thr	Thr	Asn	Tyr	
65					70				75						80	
aat ccc tcc ctc aag agt cga gtc acc att tca aaa gac acg tcc aag															288	

Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	
				85					90						95	
aac	cag	ttc	ttc	ctg	aac	ttg	aat	tct	gtg	acc	gac	gcg	gac	acg	gcc	336
Asn	Gln	Phe	Phe	Leu	Asn	Leu	Asn	Ser	Val	Thr	Asp	Ala	Asp	Thr	Ala	
			100					105					110			
gtc	tat	tac	tgt	gcg	aga	ggc	cct	cg	cct	gat	tgc	aca	acc	att	tgt	384
Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Pro	Arg	Pro	Asp	Cys	Thr	Thr	Ile	Cys	
			115				120					125				
tat	ggc	ggc	tgg	gtc	gat	gtc	tgg	ggc	ccg	gga	gac	ctg	gtc	acc	gtc	432
Tyr	Gly	Gly	Trp	Val	Asp	Val	Trp	Gly	Pro	Gly	Asp	Leu	Val	Thr	Val	
	130						135				140					
tcc	tca	gct	agc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca	ccc	tcc	480
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	
145					150					155					160	
tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	528
Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
				165					170					175		
gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	576
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
			180					185					190			
acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	624
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
			195				200					205				
tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	672
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
	210						215					220				
cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	720
Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	
225					230					235					240	
gac	aag	aaa	gca	gag	ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	768
Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	
				245					250					255		
ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	816
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	
			260					265					270			
ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	864
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	
		275					280					285				
aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	912
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	
	290					295					300					
aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	960
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
305						310					315				320	
cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	1008

Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr		
				325					330					335			
gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	1056	
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val		
			340					345					350				
tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	1104	
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala		
		355					360					365					
aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	1152	
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg		
	370					375					380						
gat	gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	1200	
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly		
385					390				395					400			
ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	1248	
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro		
				405				410						415			
gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	1296	
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser		
			420					425					430				
ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	1344	
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln		
		435					440					445					
ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	1392	
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His		
	450					455					460						
tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggc	aaa	tga				1431	
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
465					470					475							

<210> 4
 <211> 476
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15
 Val Leu Ser Gln Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln
 20 25 30
 Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile
 35 40 45
 Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly
 50 55 60
 Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr
 65 70 75 80

Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	
				85					90					95		
Asn	Gln	Phe	Phe	Leu	Asn	Leu	Asn	Ser	Val	Thr	Asp	Ala	Asp	Thr	Ala	
			100					105					110			
Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Pro	Arg	Pro	Asp	Cys	Thr	Thr	Ile	Cys	
		115					120					125				
Tyr	Gly	Gly	Trp	Val	Asp	Val	Trp	Gly	Pro	Gly	Asp	Leu	Val	Thr	Val	
	130					135					140					
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	
145					150					155					160	
Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
				165					170					175		
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
			180					185					190			
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
		195					200					205				
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
	210					215					220					
Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	
225					230					235					240	
Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	
				245					250					255		
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	
			260					265					270			
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	
		275					280					285				
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	
	290					295					300					
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
305					310					315					320	
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	
				325					330					335		
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	
			340					345					350			
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	
		355					360					365				
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	
	370					375					380					
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	
385					390					395					400	

Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
				405					410					415	
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
			420					425					430		
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln
		435					440					445			
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
	450					455					460				
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys				
465					470					475					

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg	480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
145 150 155 160	
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat	528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
165 170 175	
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac	576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
180 185 190	
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa	624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
195 200 205	
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag	672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
210 215 220	
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tga	720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
225 230 235	
<210> 6	
<211> 239	
<212> PRT	
<213> Homo sapiens	
<400> 6	
Met Ser Leu Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys Val Pro	
1 5 10 15	
Gly Ser Ser Gly Glu Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro	
20 25 30	
Ile Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser	
35 40 45	
Leu Lys His Ser Asn Gly Asp Thr Phe Leu Ser Trp Tyr Gln Gln Lys	
50 55 60	
Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Asp	
65 70 75 80	
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe	
85 90 95	
Thr Leu Lys Ile Ser Ala Val Glu Ala Glu Asp Val Gly Val Tyr Phe	
100 105 110	
Cys Gly Gln Gly Thr Arg Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys	
115 120 125	
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
130 135 140	
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
145 150 155 160	

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 165 170 175
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 180 185 190
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 195 200 205
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 210 215 220
 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 7
 <211> 1437
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1434)

<400> 7
 atg ggt tgg agc ctc atc ttg ctc ttc ctt gtc gct gtt gct acg cgt 48
 Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
 1 5 10 15
 gtc cag tgt gag gtg caa ctg gtg gag tct ggg gga ggc ttg gtc cag 96
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30
 cct ggc ggg tcc ctg aga gtc tcc tgt gca gtc tct gga ttc acc ttc 144
 Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Val Ser Gly Phe Thr Phe
 35 40 45
 agt gac cac tac atg tat tgg ttc cgc cag gct cca ggg aag ggg ccg 192
 Ser Asp His Tyr Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Pro
 50 55 60
 gaa tgg gta ggt ttc att aga aac aaa ccg aac ggt ggg aca aca gaa 240
 Glu Trp Val Gly Phe Ile Arg Asn Lys Pro Asn Gly Gly Thr Thr Glu
 65 70 75 80
 tac gcc gcg tct gtg aaa gac aga ttc acc atc tcc aga gat gat tcc 288
 Tyr Ala Ala Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
 85 90 95
 aaa agc atc gcc tat ctg caa atg agc agc ctg aaa atc gag gac acg 336
 Lys Ser Ile Ala Tyr Leu Gln Met Ser Ser Leu Lys Ile Glu Asp Thr
 100 105 110
 gcc gtc tat tac tgt act aca tcc tac att tca cat tgt cgg ggt ggt 384
 Ala Val Tyr Tyr Cys Thr Thr Ser Tyr Ile Ser His Cys Arg Gly Gly
 115 120 125
 gtc tgc tat gga ggt tac ttc gaa ttc tgg ggc cag ggc gcc ctg gtc 432
 Val Cys Tyr Gly Gly Tyr Phe Glu Phe Trp Gly Gln Gly Ala Leu Val

130	135	140	
acc gtc tcc tca gct agc Thr Val Ser Ser Ala Ser 145	acc aag ggc cca tgc Thr Lys Gly Pro Ser 150	gtc ttc ccc ctg gca Val Phe Pro Leu Ala 155	480
ccc tcc tcc aag agc Pro Ser Ser Lys Ser 165	tct ggg ggc aca gcg Ser Gly Gly Thr Ala 170	gcc ctg ggc tgc ctg Ala Ala Leu Gly Cys 175	528
gtc aag gac tac ttc Val Lys Asp Tyr Phe 180	ccc gaa ccg gtg acg Pro Glu Pro Val Thr 185	gtg tgc tgg aac tca ggc Ser Trp Asn Ser Gly 190	576
gcc ctg acc agc ggc Ala Leu Thr Ser Gly 195	gtg cac acc ttc ccg Val His Thr Phe Pro 200	gct gtc cta cag tcc tca Ala Val Leu Gln Ser 205	624
gga ctc tac tcc ctc Gly Leu Tyr Ser Leu 210	agc agc gtg gtg acc Ser Val Val Thr Val 215	gtg ccc tcc agc agc ttg Pro Ser Ser Ser Leu 220	672
ggc acc cag acc tac Gly Thr Gln Thr Tyr 225	atc tgc aac gtg aat Ile Cys Asn Val Asn 230	cac aag ccc agc aac acc His Lys Pro Ser Asn Thr 235	720
aag gtg gac aag aaa Lys Val Asp Lys Lys 245	gca gag ccc aaa tct Ala Glu Pro Lys Ser 250	gtg gac aaa act cac aca Cys Asp Lys Thr His Thr 255	768
tgc cca ccg tgc cca Cys Pro Pro Cys Pro 260	gca cct gaa ctc ctg Ala Pro Glu Leu Leu 265	ggg gga ccg tca gtc ttc Gly Gly Pro Ser Val Phe 270	816
ctc ttc ccc cca aaa Leu Phe Pro Pro Lys 275	ccc aag gac acc ctc Pro Lys Asp Thr Leu 280	atg atc tcc cgg acc cct Met Ile Ser Arg Thr Pro 285	864
gag gtc aca tgc gtg Glu Val Thr Cys Val 290	gtg gtg gac gtg agc Val Val Asp Val Ser 295	cac gaa gac cct gag gtc His Glu Asp Pro Glu Val 300	912
aag ttc aac tgg tac Lys Phe Asn Trp Tyr 305	gtg gac ggc gtg gag Val Asp Gly Val Glu 310	gtg cat aat gcc aag aca Val His Asn Ala Lys Thr 315	960
aag ccg cgg gag gag Lys Pro Arg Glu Glu 325	cag tac aac agc acg Gln Tyr Asn Ser Thr 330	tac cgt gtg gtc agc gtc Tyr Arg Val Val Ser Val 335	1008
ctc acc gtc ctg cac Leu Thr Val Leu His 340	cag gac tgg ctg aat Gln Asp Trp Leu Asn 345	ggc aag gag tac aag tgc Gly Lys Glu Tyr Lys Cys 350	1056
aag gtc tcc aac aaa Lys Val Ser Asn Lys 355	gcc ctc cca gcc ccc Ala Leu Pro Ala Pro 360	atc gag aaa acc atc tcc Ile Glu Lys Thr Ile Ser 365	1104
aaa gcc aaa ggg cag Lys Ala Lys Gly Gln 370	ccc cga gaa cca cag Pro Arg Glu Pro Gln 375	gtg tac acc ctg ccc cca Val Tyr Thr Leu Pro Pro 380	1152

tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc 1200
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 385 390 395 400

aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg 1248
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 405 410 415

cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac 1296
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 420 425 430

ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg 1344
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 435 440 445

cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac 1392
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 450 455 460

aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga 1437
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 465 470 475

<210> 8

<211> 478

<212> PRT

<213> Homo sapiens

<400> 8

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
 1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30

Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Val Ser Gly Phe Thr Phe
 35 40 45

Ser Asp His Tyr Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Pro
 50 55 60

Glu Trp Val Gly Phe Ile Arg Asn Lys Pro Asn Gly Gly Thr Thr Glu
 65 70 75 80

Tyr Ala Ala Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
 85 90 95

Lys Ser Ile Ala Tyr Leu Gln Met Ser Ser Leu Lys Ile Glu Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Thr Thr Ser Tyr Ile Ser His Cys Arg Gly Gly
 115 120 125

Val Cys Tyr Gly Gly Tyr Phe Glu Phe Trp Gly Gln Gly Ala Leu Val
 130 135 140

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala

145					150						155				160
Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu
				165					170					175	
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly
			180					185					190		
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser
		195					200					205			
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu
	210					215					220				
Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr
225					230					235					240
Lys	Val	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr
				245					250					255	
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
			260					265						270	
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
		275					280					285			
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
	290					295					300				
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
305					310						315				320
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
				325					330					335	
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
			340					345					350		
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
		355					360					365			
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
	370					375					380				
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
385					390					395					400
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
				405					410					415	
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
			420					425					430		
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
		435					440					445			
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
	450					455					460				
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys		
465					470					475					

<210> 9
 <211> 711
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (708)

<400> 9
 atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc ccā 48
 Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

ggt gca cga tgt gag tct gcc ctg aca cag ccg ccc tca gtg tct ggg 96
 Gly Ala Arg Cys Glu Ser Ala Leu Thr Gln Pro Pro Ser Val Ser Gly
 20 25 30

gcc cca ggg cag aag gtc acc atc tcg tgc act ggg agc acc tcc aac 144
 Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asn
 35 40 45

att gga ggt tat gat cta cat tgg tac cag cag ctc cca gga acg gcc 192
 Ile Gly Gly Tyr Asp Leu His Trp Tyr Gln Gln Leu Pro Gly Thr Ala
 50 55 60

ccc aaa ctc ctc atc tat gac att aac aag cga ccc tca gga att tct 240
 Pro Lys Leu Leu Ile Tyr Asp Ile Asn Lys Arg Pro Ser Gly Ile Ser
 65 70 75 80

gac cga ttc tct ggc tcc aag tct ggt acc gcg gcc tcc ctg gcc atc 288
 Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile
 85 90 95

act ggg ctc cag act gag gat gag gct gat tat tac tgc cag tcc tat 336
 Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
 100 105 110

gac agc agc ctg aat gct cag gta ttc gga gga ggg acc cgg ctg acc 384
 Asp Ser Ser Leu Asn Ala Gln Val Phe Gly Gly Gly Thr Arg Leu Thr
 115 120 125

gtc cta ggt cag ccc aag gct gcc ccc acg gtc act ctg ttc ccg ccc 432
 Val Leu Gly Gln Pro Lys Ala Ala Pro Thr Val Thr Leu Phe Pro Pro
 130 135 140

tcc tct gag gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata 480
 Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile
 145 150 155 160

agt gac ttc tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc 528
 Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser
 165 170 175

agc ccc gtc aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc 576
 Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser
 180 185 190

aac aac aag tac gcg gcc agc agc tac ctg agc ctg acg cct gag cag 624

Asn	Asn	Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln		
		195					200					205					
tgg	aag	tcc	cac	aga	agc	tac	agc	tgc	cag	gtc	acg	cat	gaa	ggg	agc	672	
Trp	Lys	Ser	His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser		
	210					215					220						
acc	gtg	gag	aag	aca	gtg	gcc	cct	aca	gaa	tgt	tca	tga				711	
Thr	Val	Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser						
225					230					235							

<210> 10
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu Pro
 1 5 10 15
 Gly Ala Arg Cys Glu Ser Ala Leu Thr Gln Pro Pro Ser Val Ser Gly
 20 25 30
 Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asn
 35 40 45
 Ile Gly Gly Tyr Asp Leu His Trp Tyr Gln Gln Leu Pro Gly Thr Ala
 50 55 60
 Pro Lys Leu Leu Ile Tyr Asp Ile Asn Lys Arg Pro Ser Gly Ile Ser
 65 70 75 80
 Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile
 85 90 95
 Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
 100 105 110
 Asp Ser Ser Leu Asn Ala Gln Val Phe Gly Gly Gly Thr Arg Leu Thr
 115 120 125
 Val Leu Gly Gln Pro Lys Ala Ala Pro Thr Val Thr Leu Phe Pro Pro
 130 135 140
 Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile
 145 150 155 160
 Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser
 165 170 175
 Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser
 180 185 190
 Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln
 195 200 205
 Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser
 210 215 220

Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
 225 230 235

<210> 11
 <211> 1431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1428)

<400> 11
 atg aaa cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg 48
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15
 gtc ctg tcc cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag 96
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 20 25 30
 cct tcg gag acc ctg tcc ctc acc tgc gct gtc tct ggt ggc tcc atc 144
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile
 35 40 45
 agc ggt ggt tat ggc tgg ggc tgg atc cgc cag ccc cca ggg aag ggg 192
 Ser Gly Gly Tyr Gly Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly
 50 55 60
 ctg gag tgg att ggg agt ttc tat agt agt agt ggg aac acc tac tac 240
 Leu Glu Trp Ile Gly Ser Phe Tyr Ser Ser Ser Gly Asn Thr Tyr Tyr
 65 70 75 80
 aac ccc tcc ctc aag agt caa gtc acc att tca aca gac acg tcc aag 288
 Asn Pro Ser Leu Lys Ser Gln Val Thr Ile Ser Thr Asp Thr Ser Lys
 85 90 95
 aac cag ttc tcc ctg aag ctg aac tct atg acc gcc gcg gac acg gcc 336
 Asn Gln Phe Ser Leu Lys Leu Asn Ser Met Thr Ala Ala Asp Thr Ala
 100 105 110
 gtg tat tac tgt gtg aga gat cgt ctt ttt tca gtt gtt gga atg gtt 384
 Val Tyr Tyr Cys Val Arg Asp Arg Leu Phe Ser Val Val Gly Met Val
 115 120 125
 tac aac aac tgg ttc gat gtc tgg ggc ccg gga gtc ctg gtc acc gtc 432
 Tyr Asn Asn Trp Phe Asp Val Trp Gly Pro Gly Val Leu Val Thr Val
 130 135 140
 tcc tca gct agc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc 480
 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 145 150 155 160
 tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag 528
 Ser Lys Ser Thr Ser Gly Gly Thr Ala Leu Gly Cys Leu Val Lys
 165 170 175
 gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg 576
 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
 180 185 190

acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc	624
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
195 200 205	
tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc	672
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
210 215 220	
cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg	720
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
225 230 235 240	
gac aag aaa gca gag ccc aaa tct tgt gac aaa act cac aca tgc cca	768
Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro	
245 250 255	
ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc	816
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe	
260 265 270	
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc	864
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
275 280 285	
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc	912
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	
290 295 300	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg	960
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
305 310 315 320	
cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc	1008
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	
325 330 335	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc	1056
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
340 345 350	
tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc	1104
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala	
355 360 365	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg	1152
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	
370 375 380	
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc	1200
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	
385 390 395 400	
ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg	1248
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro	
405 410 415	
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gag ggc tcc	1296
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser	
420 425 430	

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag	1344
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln	
435 440 445	
ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac	1392
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His	
450 455 460	
tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga	1431
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
465 470 475	

<210> 12
 <211> 476
 <212> PRT
 <213> Homo sapiens

<400> 12	
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
1 5 10 15	
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys	
20 25 30	
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile	
35 40 45	
Ser Gly Gly Tyr Gly Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly	
50 55 60	
Leu Glu Trp Ile Gly Ser Phe Tyr Ser Ser Ser Gly Asn Thr Tyr Tyr	
65 70 75 80	
Asn Pro Ser Leu Lys Ser Gln Val Thr Ile Ser Thr Asp Thr Ser Lys	
85 90 95	
Asn Gln Phe Ser Leu Lys Leu Asn Ser Met Thr Ala Ala Asp Thr Ala	
100 105 110	
Val Tyr Tyr Cys Val Arg Asp Arg Leu Phe Ser Val Val Gly Met Val	
115 120 125	
Tyr Asn Asn Trp Phe Asp Val Trp Gly Pro Gly Val Leu Val Thr Val	
130 135 140	
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser	
145 150 155 160	
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys	
165 170 175	
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu	
180 185 190	
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
195 200 205	
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
210 215 220	

Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	225	230	235	240
Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	245	250	255	
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	260	265	270	
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	275	280	285	
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	290	295	300	
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	305	310	315	320
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	325	330	335	
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	340	345	350	
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	355	360	365	
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	370	375	380	
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	385	390	395	400
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	405	410	415	
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	420	425	430	
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	435	440	445	
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	450	455	460	
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					465	470	475	